WEST Search History

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DATE: Wednesday, October 03, 2007

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	DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; PLUR=YES; OP=ADJ		
☐	L15	zif268 and L12	1
☐	L13	(catalytic or (DNA with binding)) same L9	2
☐	L12	(catalytic or (DNA with binding)) and L9	13
☐	L9	domain same L3	15
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☐	L7	TN3 same L3	3
☐	L6	(G101 or Q105 or V107 or A117 or R121 or E124 or A89 or F92 or M103) and L3	3
☐	L5	(G101 or Q105 or V107) and L3	3
☐	L4	(G101 or Q105 or V107) same L3	1
☐	L3	(hyperactive or hybrid) same L2	78
☐	L2	(mutant or variant or recombinant or mutat$3) same L1	2563
☐	L1	(recombinase or resolvase)	8602

END OF SEARCH HISTORY

=> index bioscience medicine

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE, AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB, DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 14:49:45 ON 03 OCT 2007

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=> S (recombinase or resolvase)
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1071 FILE BIOTECHDS
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455 FILE CABA
4579 FILE CAPLUS
58 FILE CEABA-VTB
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62 FILE CONFSCI
4 FILE CROPU
1 FILE DDFB
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11096 FILE DGENE
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57 FILE NTIS
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1048 FILE PASCAL
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67 FILE PROMT
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2023 FILE TOXCENTER
1139 FILE USGENE
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997 FILE USPAT2
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867 FILE WPINDEX
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L1 QUE (RECOMBINASE OR RESOLVASE)

=> d rank

F1 124043 GENBANK
F2 11096 DGENE
F3 6396 USPATFULL
F4 5004 MEDLINE
F5 4579 CAPLUS
F6 4545 BIOSIS
F7 4139 EMBASE
F8 4062 SCISEARCH
F9 2644 LIFESCI
F10 2569 ESBIOBASE
F11 2189 BIOTECHNO
F12 2023 TOXCENTER
F13 1139 USGENE
F14 1071 BIOTECHABS
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F16 1048 PASCAL
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F19 867 WPIDS
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F24 296 AGRICOLA
F25 82 NLDB

=> file f3-f12, f14, f16, f19

FILE 'USPATFULL' ENTERED AT 14:51:18 ON 03 OCT 2007
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FILE 'WPIDS' ENTERED AT 14:51:18 ON 03 OCT 2007
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=> S L1
L2 40065 L1

=> S (serine or TN3)(s) L2
L3 1468 (SERINE OR TN3)(S) L2

=> S (hyperactive or hybrid) (s) L3
L4 45 (HYPERACTIVE OR HYBRID) (S) L3

=> S (mutant or variant or recombinant or mutat?) (s) L4
L5 14 (MUTANT OR VARIANT OR RECOMBINANT OR MUTAT?) (S) L4

=> S (G101 or Q105 or V107)(s) L5
L6 2 (G101 OR Q105 OR V107)(S) L5

=> S (G101 or Q105 or V107)and L5
L7 2 (G101 OR Q105 OR V107) AND L5

=> S (G101 or Q105 or V107) and L5
L8 2 (G101 OR Q105 OR V107) AND L5

=> dup rem L5
PROCESSING COMPLETED FOR L5
L9 10 DUP REM L5 (4 DUPLICATES REMOVED)

=> d ibib abs L9 1-10

L9 ANSWER 1 OF 10 WPIDS COPYRIGHT 2007 THE THOMSON CORP on STN
ACCESSION NUMBER: 2007-192549 [19] WPIDS
DOC. NO. CPI: C2007-069962 [19]
TITLE: Generating transgenic Zea mays, by introducing DNA construct having sequence encoding enzyme that metabolizes D-alanine/D-serine, and conferring agronomically trait into Z.mays cell/tissue, and regenerating cell/tissue into plants
DERWENT CLASS: B04; C06; D16
INVENTOR: JONES T; LAI F; MANKIN L; MEI K; SONG H
PATENT ASSIGNEE: (BADI-C) BASF PLANT SCI GMBH
COUNTRY COUNT: 113

PATENT INFO ABBR.:

PATENT NO	KIND	DATE	WEEK	LA	PG	MAIN IPC
WO 2007014844	A2	20070208	(200719)*	EN	86[2]	

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2007014844	A2	WO 2006-EP64356	20060718

PRIORITY APPLN. INFO: US 2005-702934P 20050727
AN 2007-192549 [19] WPIDS
AB WO 2007014844 A2 UPAB: 20070319
NOVELTY - Generating transgenic Zea mays plant, involves introducing into Z.mays cell/tissue, a DNA construct comprising first construct having nucleic acid encoding enzyme that metabolizes D-alanine and/or D-serine linked to ubiquitin promoter, and second construct conferring agronomically valuable trait to the plant; incubating the cell/tissue on a selection medium comprising D-alanine, D-serine and/or their derivative for at least 5 days; and transferring cell/tissue to regeneration medium and regenerating and selecting plants comprising the construct.
DETAILED DESCRIPTION - Generating a transgenic Zea mays plant, involves introducing into a Z.mays cell or tissue a DNA construct comprising at least one first expression construct comprising a nucleic acid sequence encoding an enzyme capable of metabolizing D-alanine and/or D-serine operably linked to a ubiquitin promoter, and at least one second expression construct conferring to the Z.mays plant an agronomically

valuable trait; incubating the Z.mays cell or tissue on a selection medium comprising D-alanine and/or D-serine and/or their derivative in a total concentration from 1-100 mM for a time period of at least 5 days; and transferring the Z.mays cell or tissue to a regeneration medium and regenerating and selecting Z.mays plants comprising the DNA construct. INDEPENDENT CLAIMS are included for the following: (1) a recombinant expression construct (C1) comprising a nucleic acid sequence encoding an enzyme capable of metabolizing D-alanine or D-serine operably linked to an ubiquitin promoter, where the promoter is heterologous in relation to the enzyme encoding sequence; (2) a DNA construct (C2) comprising at least one first expression construct comprising a nucleic acid sequence encoding an enzyme capable of metabolizing D-alanine and/or D-serine operably linked to an ubiquitin promoter, and at least one second expression construct conferring to the Z.mays plant an agronomically valuable trait; (3) a vector comprising (C1) or (C2); (4) a transgenic cell or non-human organism, comprising (C1), (C2), or the vector;.(5) a descendant plant of the above non-human organism; (6) a hybrid plant produced from the above non-human organism or descendant plant; (7) an inbred plant produced from the above non-human organism or descendant plant; (8) a part of the above plants; (9) a method for subsequent transformation of at least two DNA constructs into a Z.mays plant, involves (a) performing transformation with a first construct comprising at least one expression construct comprising a nucleic acid sequence encoding an enzyme capable of metabolizing D-alanine or D-serine operably linked to a ubiquitin promoter, and performing transformation with a second construct the construct comprising a second selection marker gene, which is not conferring resistance against D-alanine or D-serine, or (b) performing transformation with a first construct comprising a expression construct comprising a nucleic acid sequence encoding an D-serine dehydratase (dsdA) enzyme operably linked to a plant promoter and selecting with D-serine, and performing transformation with a second construct comprising a expression construct comprising a nucleic acid sequence encoding a D-amino acid oxidase (dao) enzyme operably linked to a plant promoter and selecting with D-alanine; and (10) maize plant comprising a first expression construct comprising a nucleic acid sequence encoding an enzyme capable of metabolizing D-alanine or D-serine operably linked to a ubiquitin promoter, and a second expression construct for a selection marker gene, which is not conferring resistance against D-alanine or D-serine.

USE - For generating a transgenic Z.mays plant (claimed).

DESCRIPTION OF DRAWINGS - The figure shows graph representing the effect of D-alanine on inhibiting the germination of dissected immature embryos of corn J553x (HillAxA188).

L9 ANSWER 2 OF 10 LIFESCI COPYRIGHT 2007 CSA on STN DUPLICATE 1
ACCESSION NUMBER: 2007:195252 LIFESCI <<LOGINID::20071003>>
TITLE: Sequences in attB that affect the ability of {phi}C31 integrase to synapse and to activate DNA cleavage
AUTHOR: Gupta, Milind; Till, Rob; Smith, Margaret C. M.
CORPORATE SOURCE: Institute of Medical Sciences, University of Aberdeen, Foresterhill, Aberdeen AB25 2ZD and Institute of Genetics, Queens Medical Centre, University of Nottingham, Nottingham NG7 2UH, UK
SOURCE: Nucleic Acids Research [Nucleic Acids Res.], (20070500) vol. 35, no. 10, pp. 3407-3419.
ISSN: 0305-1048.
DOCUMENT TYPE: Journal
FILE SEGMENT: N
LANGUAGE: English
SUMMARY LANGUAGE: English

AB Phage integrases are required for recombination of the phage genome with the host chromosome either to establish or exit from the lysogenic state. {phi}C31 integrase is a member of the ***serine*** ***recombinase*** family of site-specific recombinases. In the absence of any accessory factors integrase is unidirectional, catalysing the integration reaction between the phage and host attachment sites, attP x attB to generate the ***hybrid*** sites, attL and attR. The basis for this directionality is due to selective synapsis of attP and attB sites. Here we show that ***mutations*** in attB can block the integration reaction at different stages. ***Mutations*** at positions distal to the crossover site

inhibit recombination by destabilizing the synapse with attP without significantly affecting DNA-binding affinity. These data are consistent with the proposal that integrase adopts a specific conformation on binding to attB that permits synapsis with attP. Other attB mutants with changes close to the crossover site are able to form a stable synapse but cleavage of the substrates is prevented. These mutants indicate that there is a post-synaptic DNA recognition event that results in activation of DNA cleavage.

L9 ANSWER 3 OF 10 USPATFULL on STN
ACCESSION NUMBER: 2006:202489 USPATFULL <<LOGINID::20071003>>
TITLE: Mutant Recombinases
INVENTOR(S): Stark, William Marshall, Glasgow, Central Scotland, UNITED KINGDOM
Akopian, Aram, Glasgow, Central Scotland, UNITED KINGDOM
PATENT ASSIGNEE(S): The University Court of the University of Glasgow, Glasgow, Central Scotland, UNITED KINGDOM, G12 8QQ (non-U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2006172373	A1	20060803
APPLICATION INFO.:	US 2003-529059	A1	20030925 (10)
	WO 2003-GB4169		20030925
			20051214 PCT 371 date

	NUMBER	DATE
PRIORITY INFORMATION:	GB 2002-22229	20020925

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: MORGAN LEWIS & BOCKIUS LLP, 1111 PENNSYLVANIA AVENUE NW, WASHINGTON, DC, 20004, US
NUMBER OF CLAIMS: 69
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 13 Drawing Page(s)
LINE COUNT: 2368
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention provides hyperactive mutant recombinases and hybrid mutant recombinases, and methods for their identification. Also provided are nucleic acids encoding hyperactive mutant recombinases and hybrid recombinases, as well as vectors and host cells. Host cells include eukaryotic cells capable of expressing said recombinases and carrying out site-specific recombination in the cell. The mutant recombinases may be used, for example, in biotechnology, gene therapy or transgenic applications.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L9 ANSWER 4 OF 10 USPATFULL on STN
ACCESSION NUMBER: 2006:92851 USPATFULL <<LOGINID::20071003>>
TITLE: Production of polyketides and other natural products
INVENTOR(S): Gregory, Matthew Alan, Cambridge, UNITED KINGDOM
Gaisser, Sabine, Cambridge, UNITED KINGDOM
Petkovic, Hrvoje, Cambridge, UNITED KINGDOM
Moss, Steven, Cambridge, UNITED KINGDOM

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2006078980	A1	20060413
APPLICATION INFO.:	US 2005-269215	A1	20051108 (11)

RELATED APPLN. INFO.: Continuation of Ser. No. US 2005-497135, filed on 23 Mar 2005, PENDING A 371 of International Ser. No. WO 2003-GB3230, filed on 16 Jul 2003

	NUMBER	DATE
PRIORITY INFORMATION:	GB 2002-16509	20020716
	GB 2002-24922	20021025

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: DANN, DORFMAN, HERRELL & SKILLMAN, 1601 MARKET STREET, SUITE 2400, PHILADELPHIA, PA, 19103-2307, US
NUMBER OF CLAIMS: 5
EXEMPLARY CLAIM: 1-66
NUMBER OF DRAWINGS: 38 Drawing Page(s)
LINE COUNT: 6800
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to production of polyketides and other natural products and to libraries of compounds and individual novel compounds. One important area is the isolation and potential use of novel FKBP-ligand analogues and host cells that produce these compounds. The invention is particularly concerned with methods for the efficient transformation of strains that produce FKBP analogues and recombinant cells in which cloned genes or gene cassettes are expressed to generate novel compounds such as polyketide (especially rapamycin) FKBP-ligand analogues, and to processes for their preparation, and to means employed therein (e.g. nucleic acids, vectors, gene cassettes and genetically modified strains).

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L9 ANSWER 5 OF 10 USPATFULL on STN
ACCESSION NUMBER: 2005:312515 USPATFULL <<LOGINID::20071003>>
TITLE: Production of polyketides and other natural products
INVENTOR(S): Gregory, Matthew Alan, Cambridge, UNITED KINGDOM
Gaisser, Sabine, Cambridge, UNITED KINGDOM
Petkovic, Hrvoje, Cambridge, UNITED KINGDOM
Moss, Steven, Cambridge, UNITED KINGDOM

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2005272132	A1	20051208
APPLICATION INFO.:	US 2003-497135	A1	20030716 (10)
	WO 2003-GB3230		20030716
			20050323 PCT 371 date

	NUMBER	DATE
PRIORITY INFORMATION:	GB 2002-16509	20020716
	GB 2003-224922	20021025

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: DANN, DORFMAN, HERRELL & SKILLMAN, 1601 MARKET STREET, SUITE 2400, PHILADELPHIA, PA, 19103-2307, US
NUMBER OF CLAIMS: 97
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 38 Drawing Page(s)
LINE COUNT: 7727
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to production of polyketides and other natural products and to libraries of compounds and individual novel compounds. One important area is the isolation and potential use of novel FKBP-ligand analogues and host cells that produce these compounds. The invention is particularly concerned with methods for the efficient transformation of strains that produce FKBP analogues and recombinant cells in which cloned genes or gene cassettes are expressed to generate novel compounds such as polyketide (especially rapamycin) FKBP-ligand analogues, and to processes for their,preparation, and to means employed therein (e.g. nucleic acids, vectors, gene cassettes and genetically modified strains).

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L9 ANSWER 6 OF 10 USPATFULL on STN
ACCESSION NUMBER: 2005:105073 USPATFULL <<LOGINID::20071003>>
TITLE: Cloning vectors and method for molecular cloning
INVENTOR(S): Hayashizaki, Yoshihide, Ibaraki, JAPAN
Carninci, Piero, Ibaraki, JAPAN

NUMBER KIND DATE
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PATENT INFORMATION: US 2005090010 A1 20050428
APPLICATION INFO.: US 2003-469508 A1 20020225 (10)
WO 2002-JP1667 20020225

NUMBER DATE
---------- --------
PRIORITY INFORMATION: JP 2001-57794 20010302
DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: BIRCH STEWART KOLASCH & BIRCH, PO BOX 747, FALLS CHURCH, VA, 22040-0747, US
NUMBER OF CLAIMS: 141
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 18 Drawing Page(s)
LINE COUNT: 3716
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention discloses a family of cloning vectors capable of cloning nucleic acid inserts of interest of long sizes, with low or reduced background and high efficiency of excision and method for preparing these vectors and library thereof. As example, it is disclosed a cloning vector comprising a construction vector segment (CS) and a replaceable segment (RS), wherein the size of CS is: 36.5 kb.ltoreq.CS<38 kb, preferably CS is 37.5 kb, comprising lox recombination sites for Cre-recombination and/or att recombination sites for Gateway-like recombination, preferably also a background-reducing system selected from the group of: the ccdB gene, a lox sequence, the lacZ gene, and asymmetric site sequences recognized by restriction endonucleases.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L9 ANSWER 7 OF 10 USPATFULL on STN
ACCESSION NUMBER: 2005:98948 USPATFULL <<LOGINID::20071003>>
TITLE: Novel method for detecting and analyzing protein interactions in vivo
INVENTOR(S): Rossner, Moritz, Goettingen, GERMANY, FEDERAL REPUBLIC OF
Laage, Rico, Schriesheim, GERMANY, FEDERAL REPUBLIC OF
Nave, Klaus-Armin, Goettingen, GERMANY, FEDERAL REPUBLIC OF
Gruenewald, Sylvia, Heidelberg, GERMANY, FEDERAL REPUBLIC OF
PATENT ASSIGNEE(S): AXARON BIOSCIENCE AG, Gottingen, GERMANY, FEDERAL REPUBLIC OF (non-U.S. corporation)

NUMBER KIND DATE
---------- ------ --------
PATENT INFORMATION: US 2005084864 A1 20050421
APPLICATION INFO.: US 2003-507506 A1 20030313 (10)
WO 2003-EP2611 20030313

NUMBER DATE
---------- --------
PRIORITY INFORMATION: DE 2002-10211063 20020313
DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: FOLEY AND LARDNER, SUITE 500, 3000 K STREET NW, WASHINGTON, DC, 20007, US
NUMBER OF CLAIMS: 60
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 25 Drawing Page(s)
LINE COUNT: 3424
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention relates to a method of detecting and analyzing protein interactions in a cell, which comprises the steps: d) provision of the activity of at least one enzyme from the group consisting of recombinases and proteases in the cell as a result of a protein interaction, e) continual generation of an active reporter protein in

the cell in question as a result of the enzymic activity of step a) for a period of time which exceeds the duration of the protein interaction of step a), f) generation of a detection signal by the reporter proteins generated in b). The invention furthermore relates to reverse embodiments of the method above of detecting and analyzing protein interactions in a cell, with, as a result of the induced dissociation of a defined interaction between proteins, the activity of at least one enzyme from the group consisting of recombinases and proteases being provided in the cell and converted to a permanent detection signal of said cell. The invention moreover relates to cells expressing the protein components of the invention and to kits providing the protein components of the invention at the DNA level in the form of suitable expression vectors and, where appropriate, suitable transfectable or injectable cells. The cells provided may, where appropriate, express stably or transiently individual protein components of the invention.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L9 ANSWER 8 OF 10 WPIDS COPYRIGHT 2007 THE THOMSON CORP on STN
ACCESSION NUMBER: 2004-316113 [29] WPIDS
DOC. NO. CPI: C2004-119930 [29]
TITLE: New serine recombinase having a catalytic domain mutated at Q105 and/or G101 of Tn3 resolvase, and a DNA binding domain, for use in biotechnology, gene therapy or transgenic applications
DERWENT CLASS: B04; D16
INVENTOR: AKOPIAN A; AKOPIAN A I O B; STARK W M; STARK W M I O B
PATENT ASSIGNEE: (UNIU-C) UNIV GLASGOW
COUNTRY COUNT: 105

PATENT INFO ABBR.:

PATENT NO	KIND	DATE	WEEK	LA	PG	MAIN IPC
WO 2004029233	A2	20040408 (200429)*		EN	95[10]	
AU 2003269194	A1	20040419 (200462)		EN		
EP 1546311	A2	20050629 (200543)		EN		
AU 2003269194	A8	20051110 (200634)		EN		
US 20060172373	A1	20060803 (200651)		EN		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2004029233	A2	WO 2003-GB4169	20030925
AU 2003269194	A1	AU 2003-269194	20030925
AU 2003269194	A8	AU 2003-269194	20030925
EP 1546311	A2	EP 2003-750972	20030925
EP 1546311	A2	WO 2003-GB4169	20030925
US 20060172373	A1	WO 2003-GB4169	20030925
US 20060172373	A1	US 2005-529059	20051214

FILING DETAILS:

PATENT NO	KIND		PATENT NO	
AU 2003269194	A1	Based on	WO 2004029233	A
EP 1546311	A2	Based on	WO 2004029233	A
AU 2003269194	A8	Based on	WO 2004029233	A

PRIORITY APPLN. INFO: GB 2002-22229 20020925
AN 2004-316113 [29] WPIDS
AB WO 2004029233 A2 UPAB: 20060121
NOVELTY - A serine recombinase comprising a catalytic domain and a DNA binding domain, where the catalytic domain is mutated at G101 or at a position corresponding to G101 of Tn3 resolvase, is new.
DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:
(1) a serine recombinase comprising a catalytic domain and a DNA binding domain wherein said catalytic domain is mutated at Q105 or at a

position corresponding to Q105 of Tn3 resolvase;

(2) a serine recombinase comprising a catalytic domain and a DNA binding domain wherein said catalytic domain is mutated at D102 or at a position corresponding to D102 of Tn3 resolvase, and wherein the serine recombinase is not a D102Y E124Q mutant;

(3) a nucleic acid sequence encoding any of the serine recombinases cited above, the hybrid recombinase of (7) or the catalytic domain of (8), (9) or (10);

(4) a nucleic acid expression vector comprising a nucleic acid sequence of (3);

(5) a host cell comprising a nucleic acid sequence of (3) or a nucleic acid expression vector of (4);

(6) a hybrid recombinase comprising a catalytic domain from a serine recombinase connected by way of a linker to a heterologous DNA binding domain wherein said hybrid recombinase is capable of binding nucleic acid by way of said DNA binding domain and said catalyzing recombination of said DNA;

(7) a ***hybrid*** ***recombinase*** comprising a ***Tn3*** ***resolvase*** catalytic domain, which catalytic domain comprises the ***mutations*** R2A, E56K, G101S, D102Y, M1031 and Q105L and V107F, linked to a DNA binding domain via a linker comprising the sequence TS, wherein said ***hybrid*** ***recombinase*** is capable of binding nucleic acid by way of said DNA binding domain and catalyzing recombination of said DNA;

(8) a catalytic domain of a serine recombinase which has been mutated at Gl0l or at a position corresponding to Gl0l of Tn3 resolvase;

(9) a catalytic domain of a serine recombinase which has been mutated at Q105 or at a position corresponding to Q105 of Tn3 resolvase;

(10) a catalytic domain of a serine recombinase which is mutated at D102 or at a position corresponding to D102 of Tn3 resolvase, and wherein the catalytic domain does not further comprise a mutation at E124Q;

(11) a method for identifying a ***hyperactive*** ***mutant*** ***serine*** ***recombinase*** capable of catalyzing site-specific DNA recombination when bound to a recognition site comprising fewer nucleotides than necessary for achieving recombination with a corresponding wild-type ***serine*** ***recombinase*** , comprising ***mutating*** said wild-type ***serine*** ***recombinase*** such that the ***mutant*** ***recombinase*** comprises one or more ***mutations*** , in a catalytic domain of the ***recombinase*** , with respect to the wild-type ***serine*** ***recombinase*** , and detecting whether or not said ***mutant*** ***serine*** ***recombinase*** is capable of catalyzing DNA recombination when bound to said recognition site comprising fewer nucleotides than necessary for achieving recombination with the corresponding wild-type ***serine*** ***recombinase*** ;

(12) a method of recombining DNA comprising contacting a first DNA sequence and a second DNA sequence with any of the serine recombinases cited above for allowing a recombination of said first and second DNA sequences;

(13) a kit for recombining a first DNA sequence and a second DNA sequence said kit comprising any of the serine recombinases cited above or the hybrid recombinase of (7); and

(14) a kit for recombining a first DNA sequence and a second DNA sequence, comprising a nucleic acid sequence of (3) or the expression vector of (4).

ACTIVITY - None given.

MECHANISM OF ACTION - Gene therapy.

USE - The methods and compositions of the present invention are useful in biotechnology, gene therapy or transgenic applications.

L9 ANSWER 9 OF 10 CAPLUS COPYRIGHT 2007 ACS on STN DUPLICATE 2
ACCESSION NUMBER: 2004:177170 CAPLUS <<LOGINID::20071003>>
DOCUMENT NUMBER: 140:283345
TITLE: Activating mutations of Tn3 resolvase marking interfaces important in recombination catalysis and its regulation
AUTHOR(S): Burke, Mary E.; Arnold, Patricia H.; He, Jiuya; Wenwieser, Sandra V. C. T.; Rowland, Sally J.; Boocock, Martin R.; Stark, W. Marshall

CORPORATE SOURCE: Institute of Biomedical and Life Sciences, University of Glasgow, Glasgow, G11 6NU, UK
SOURCE: Molecular Microbiology (2004), 51(4), 937-948
CODEN: MOMIEE; ISSN: 0950-382X
PUBLISHER: Blackwell Publishing Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Catalysis of DNA recombination by Tn3 resolvase is conditional on prior formation of a synapse, comprising 12 resolvase subunits and two recombination sites (res). Each res binds a resolvase dimer at site I, where strand exchange takes place, and addnl. dimers at two adjacent "accessory" binding sites II and III. "Hyperactive" resolvase mutants, that catalyze strand exchange at site I without accessory sites, were selected in E. coli. Some single mutants can resolve a res .times. site I plasmid (i.e., with one res and one site I), but two or more activating mutations are necessary for efficient resoln. of a site I .times. site I plasmid. Site I .times. site I resoln. by hyperactive mutants can be further stimulated by mutations at the crystallog. 2-3' interface that abolish activity of wild-type resolvase. Activating mutations may allow regulatory mechanisms of the wild-type system to be bypassed, by stabilizing or destabilizing interfaces within and between subunits in the synapse. The positions and characteristics of the mutations support a mechanism for strand exchange by serine recombinases in which the DNA is on the outside of a recombinase tetramer, and the tertiary/quaternary structure of the tetramer is reconfigured.

REFERENCE COUNT: 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 10 OF 10 USPATFULL on STN
ACCESSION NUMBER: 2003:108972 USPATFULL <<LOGINID::20071003>>
TITLE: Nucleic acid and amino acid sequences relating to pseudomonas aeruginosa for diagnostics and therapeutics
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PRIMARY EXAMINER: Allen, Marianne P.
LEGAL REPRESENTATIVE: Burns, Doane, Swecker & Mathis, L.L.P.
NUMBER OF CLAIMS: 26
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 0 Drawing Figure(s); 0 Drawing Page(s)
LINE COUNT: 21431
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The invention provides isolated polypeptide and nucleic acid sequences derived from Pseudomonas aeruginosa that are useful in diagnosis and therapy of pathological conditions; antibodies against the polypeptides; and methods for the production of the polypeptides. The invention also provides methods for the detection, prevention and treatment of pathological conditions resulting from bacterial infection.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

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L1 QUE (RECOMBINASE OR RESOLVASE)

L2 40065 S L1
L3 1468 S (SERINE OR TN3)(S) L2
L4 45 S (HYPERACTIVE OR HYBRID) (S) L3
L5 14 S (MUTANT OR VARIANT OR RECOMBINANT OR MUTAT?) (S) L4
L6 2 S (G101 OR Q105 OR V107)(S) L5
L7 2 S (G101 OR Q105 OR V107)AND L5
L8 2 S (G101 OR Q105 OR V107) AND L5
L9 10 DUP REM L5 (4 DUPLICATES REMOVED)

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